

# SEQUENCE LISTING

<110> FREY, Perry A.  
RUZICKA, Frank J.

<120> DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE

<130> 032026/0476

<140> US 09/330,611

<141> 1999-06-11

<150> US 09/198,942

<151> 1998-11-24

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<170> PatentIn Ver. 2.0

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Tyr Pro Asp Arg Val Leu Leu Leu Ile Thr Asp Met Cys Ser Met Tyr
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gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat	336
Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His	
100 105 110	
cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg	384
Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met	
115 120 125	
tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct	432
Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala	
130 135 140	
tct tct cct tct gag cgc atc gat cga tgc att gac tat ata gcc aat	480
Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn	
145 150 155 160	
aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ctt	528
Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu	
165 170 175	
gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata	576
Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile	
180 185 190	
cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctt	624
Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu	
195 200 205	
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat	672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His	
210 215 220	
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa	720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu	
225 230 235 240	
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg	768
Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu	
245 250 255	

ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg	816
Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val	
260 265 270	
atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac	864
Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr	
275 280 285	
tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg	912
Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr	
290 295 300	
ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc	960
Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr	
305 310 315 320	
tcg ggc tat gct gtt cct acc ttt gtg gta gat gct ccg ggg ggt ggt	1008
Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly	
325 330 335	
ggt aag ata cct gta atg ccg aac tat gtt gta tct cag tcc cca cga	1056
Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg	
340 345 350	
cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag	1104
His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu	
355 360 365	
ccg gag aat tat cat gag gag tgt gat tgt gag gac tgt cga gcc ggt	1152
Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly	
370 375 380	
aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct	1200
Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala	
385 390 395 400	
atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac	1248
Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn	
405 410 415	
tga	1251

<210> 8  
 <211> 416  
 <212> PRT  
 <213> Porphyromonas gingivalis

<400> 8  
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 Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
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 Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly  
 35 40 45  
 Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
 50 55 60  
 Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
 65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
 85 90 95  
 Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
 100 105 110  
 Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
 115 120 125  
 Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
 130 135 140  
 Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
 145 150 155 160  
 Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
 165 170 175  
 Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
 180 185 190  
 Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
 195 200 205  
 Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
 210 215 220  
 Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
 225 230 235 240  
 Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
 245 250 255  
 Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
 260 265 270  
 Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
 275 280 285  
 Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
 290 295 300  
 Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
 305 310 315 320  
 Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly  
 325 330 335  
 Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
 340 345 350  
 His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
 355 360 365  
 Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
 370 375 380  
 Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
 385 390 395 400  
 Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
 405 410 415

<210> 9  
 <211> 1416  
 <212> DNA  
 <213> Bacillus subtilis

<220>  
 <221> CDS  
 <222> (1)..(1413)

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 1 5 10 15  
 tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96  
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30  
 ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144  
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45  
 ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192  
 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60  
 ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240  
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80  
 ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288  
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95  
 cac aaa aca aaa tac gat ctg gaa gac ccg ctt cat gag gat gaa gat 336  
 His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110  
 tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384  
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125  
 ctt gtc acg aat caa tgt tcc atg tac tgc cgc tac tgc aca aga agg 432  
 Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140  
 cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480  
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160  
 gct gca att gct tat atc ccg gaa aca ccc gaa atc cgc gat tgt tta 528  
 Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175  
 att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat 576  
 Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
 180 185 190  
 att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc 624  
 Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
 195 200 205

gga aca aga gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg	672
Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu	
210 215 220	
tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt	720
Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe	
225 230 235 240	
aac aca agc atc gaa atg aca gaa gaa tcc gtt gag gca tgt gaa aag	768
Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys	
245 250 255	
ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca	816
Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala	
260 265 270	
ggt att aat gat tgc gtt cca att atg aaa aag ctc atg cat gac ttg	864
Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu	
275 280 285	
gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca	912
Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser	
290 295 300	
gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc	960
Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile	
305 310 315 320	
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt	1008
Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe	
325 330 335	
gtc gtt gac gca cca ggc gga gga ggt aaa atc gcc ctg cag cca aac	1056
Val Val Asp Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn	
340 345 350	
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa	1104
Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu	
355 360 365	
ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag	1152
Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln	
370 375 380	
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag	1200
Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys	
385 390 395 400	
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tgc ttt	1248
Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe	
405 410 415	
aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca	1296
Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala	
420 425 430	
aat ccg gag cat gaa aca tta aaa gat ccg cgt gag aaa aga gat cag	1344
Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln	
435 440 445	
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act	1392
Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr	
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gaa tgc gga ggg gat tct tca tga  
 Glu Cys Gly Gly Asp Ser Ser  
 465 470

1416

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 <211> 471  
 <212> PRT  
 <213> Bacillus subtilis

<400> 10

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Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
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Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95

His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125

Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
 180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
 195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
 210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
 225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
 245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
 260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
 275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
 290 295 300  
 Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
 305 310 315 320  
 Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
 325 330 335  
 Val Val Asp Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
 340 345 350  
 Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
 355 360 365  
 Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
 370 375 380  
 Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
 385 390 395 400  
 Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
 405 410 415  
 Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
 420 425 430  
 Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445  
 Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
 450 455 460  
 Glu Cys Gly Gly Asp Ser Ser  
 465 470

<210> 11  
 <211> 1188  
 <212> DNA  
 <213> Deinococcus radiodurans

<220>  
 <221> CDS  
 <222> (1)..(1188)

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 Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu  
 1 5 10 15  
 aag aac cgc atc aac agt gtg gag gag ttg cag gaa gtc ctg acc ctc 96  
 Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu  
 20 25 30  
 acc gag tcc gag tac cgg ggt gcg tcc gcc gag ggc att ttc cgc ctc 144  
 Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu  
 35 40 45  
 gac atc acg ccg tat ttc gcg tcc ctc atg gac ccc gaa gac ccc acc 192  
 Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr  
 50 55 60



gtg	ccg	gtg	cgc	cgt	cag	gtg	att	ccc	acc	gag	gag	gag	ctc	cag	ccg	240
Cys	Pro	Val	Arg	Arg	Gln	Val	Ile	Pro	Thr	Glu	Glu	Glu	Leu	Gln	Pro	
65					70					75					80	
ttc	acc	tcc	atg	atg	gaa	gac	tct	ctc	gcg	gag	gat	aag	cac	tcg	ccc	288
Phe	Thr	Ser	Met	Met	Glu	Asp	Ser	Leu	Ala	Glu	Asp	Lys	His	Ser	Pro	
				85					90					95		
gtg	ccg	ggg	ctg	gtg	cac	cgc	tac	ccc	gac	cgc	gtg	ctg	atg	ctg	gtc	336
Val	Pro	Gly	Leu	Val	His	Arg	Tyr	Pro	Asp	Arg	Val	Leu	Met	Leu	Val	
			100					105					110			
acg	acc	cag	tgc	gcg	agc	tac	tgc	cgc	tac	tgc	acc	cga	agc	cgc	atc	384
Thr	Thr	Gln	Cys	Ala	Ser	Tyr	Cys	Arg	Tyr	Cys	Thr	Arg	Ser	Arg	Ile	
		115					120					125				
gtg	ggc	gac	ccc	acc	gag	acg	ttc	aat	ccc	gcc	gag	tat	gag	gcg	cag	432
Val	Gly	Asp	Pro	Thr	Glu	Thr	Phe	Asn	Pro	Ala	Glu	Tyr	Glu	Ala	Gln	
	130					135					140					
ctc	aac	tac	ctg	cgc	aac	acc	ccg	cag	gtg	cgc	gac	gtg	ctg	ctt	tcc	480
Leu	Asn	Tyr	Leu	Arg	Asn	Thr	Pro	Gln	Val	Arg	Asp	Val	Leu	Leu	Ser	
145					150					155					160	
ggc	ggc	gac	ccg	ctc	aca	ctc	gcg	ccg	aag	gtg	ctg	ggg	cgc	ctg	ctt	528
Gly	Gly	Asp	Pro	Leu	Thr	Leu	Ala	Pro	Lys	Val	Leu	Gly	Arg	Leu	Leu	
				165					170					175		
tcc	gaa	ctt	cgt	aaa	atc	gag	cac	atc	gaa	atc	atc	cgc	atc	ggc	acc	576
Ser	Glu	Leu	Arg	Lys	Ile	Glu	His	Ile	Glu	Ile	Ile	Arg	Ile	Gly	Thr	
			180					185					190			
cgc	gtg	ccc	gtg	ttc	atg	ccc	atg	cgc	gtg	acc	cag	gaa	ctg	tgc	gac	624
Arg	Val	Pro	Val	Phe	Met	Pro	Met	Arg	Val	Thr	Gln	Glu	Leu	Cys	Asp	
		195					200					205				
acg	ctc	gcc	gaa	cac	cat	ccg	ctg	tgg	atg	aac	att	cac	gtc	aac	cac	672
Thr	Leu	Ala	Glu	His	His	Pro	Leu	Trp	Met	Asn	Ile	His	Val	Asn	His	
		210					215				220					
ccc	aag	gaa	atc	acc	ccc	gaa	gtg	gcc	gag	gcg	tgt	gac	cgt	ctg	acc	720
Pro	Lys	Glu	Ile	Thr	Pro	Glu	Val	Ala	Glu	Ala	Cys	Asp	Arg	Leu	Thr	
225					230					235					240	
cgc	gcg	ggc	gtg	ccg	ctc	ggc	aac	cag	agc	gtg	ctg	ctg	cgc	ggc	gtg	768
Arg	Ala	Gly	Val	Pro	Leu	Gly	Asn	Gln	Ser	Val	Leu	Leu	Arg	Gly	Val	
				245					250					255		
aac	gac	cac	ccg	gtc	atc	atg	caa	aag	ctg	ctg	cgc	gag	ctc	gtc	aaa	816
Asn	Asp	His	Pro	Val	Ile	Met	Gln	Lys	Leu	Leu	Arg	Glu	Leu	Val	Lys	
			260					265					270			
att	cgg	gtg	cgc	ccc	tac	tac	atc	tac	cag	tgc	gac	ctc	gtg	cac	ggc	864
Ile	Arg	Val	Arg	Pro	Tyr	Tyr	Ile	Tyr	Gln	Cys	Asp	Leu	Val	His	Gly	
		275					280					285				
gct	ggg	cac	ctg	cgc	acc	acg	gtc	agt	aag	ggt	ctg	gaa	atc	atg	gaa	912
Ala	Gly	His	Leu	Arg	Thr	Thr	Val	Ser	Lys	Gly	Leu	Glu	Ile	Met	Glu	
	290					295					300					
tcg	ctg	cgc	ggc	cac	acc	tcc	ggc	tac	agc	gtg	ccg	acc	tac	gtg	gtg	960
Ser	Leu	Arg	Gly	His	Thr	Ser	Gly	Tyr	Ser	Val	Pro	Thr	Tyr	Val	Val	
305					310					315					320	

gac gcg ccc ggc ggc ggc ggc aag att ccg gtg gcg ccc aac tac gtg 1008  
 Asp Ala Pro Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val  
 325 330 335

ctc tcg cac agc cct gag aag ctg att ctg cgc aac ttc gag ggc tac 1056  
 Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr  
 340 345 350

atc gcc gcc tac tcg gag ccc acc gat tac acc ggc ccc gac atg gcg 1104  
 Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala  
 355 360 365

att cct gac gac tgg att cgc aag gaa ccc ggc cag acc ggc atc ttc 1152  
 Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe  
 370 375 380

ggc ctg atg gaa ggc gag cgc att tcc atc gag ccg 1188  
 Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro  
 385 390 395

<210> 12

<211> 396

<212> PRT

<213> Deinococcus radiodurans

<400> 12

Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu  
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Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu  
 20 25 30

Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu  
 35 40 45

Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr  
 50 55 60

Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro  
 65 70 75 80

Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro  
 85 90 95

Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val  
 100 105 110

Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile  
 115 120 125

Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln  
 130 135 140

Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser  
 145 150 155 160

Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu  
 165 170 175

Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr  
 180 185 190





gga ctt gaa ata atg aga tat ttg agg gga agg ctg agc ggt ttc ggg	960
Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly	
305 310 315 320	
ata ccc act tac gcg gtg gac ctc ccg gga ggg aaa ggt aag gtt cct	1008
Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro	
325 330 335	
ctt ctt ccc aac tac gta aag aaa agg aaa ggt aat aag ttc tgg ttt	1056
Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe	
340 345 350	
gaa agt ttc acg ggt gag gtc gta gaa tac gaa gta acg gaa gta tgg	1104
Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp	
355 360 365	
gaa cct tga	1113
Glu Pro	
370	

<210> 14  
 <211> 370  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 14

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Tyr Leu Lys Leu Leu Pro Glu Glu Glu Gly Ile Lys Arg Thr Gln	
35 40 45	
Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn	
50 55 60	
Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val	
65 70 75 80	
Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu	
85 90 95	
Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg	
100 105 110	
Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys	
115 120 125	
Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu	
130 135 140	
Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg	
145 150 155 160	
Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys	
165 170 175	
Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile	
180 185 190	

Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe  
195 200 205

Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile  
210 215 220

Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu  
225 230 235 240

Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr  
245 250 255

Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu  
260 265 270

Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His  
275 280 285

Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys  
290 295 300

Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly  
305 310 315 320

Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro  
325 330 335

Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe  
340 345 350

Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp  
355 360 365

Glu Pro  
370

<210> 15  
<211> 1065  
<212> DNA  
<213> Treponema pallidum

<220>  
<221> CDS  
<222> (1)..(1065)

<400> 15  
atg tct atg gct gag tgt acc cgg gaa cag aga aag aga cga ggt gca 48  
Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala  
1 5 10 15

ggg cgt gct gat gag cat tgg cgg acg ttg agt cct gcc tct tgc gcg 96  
Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala  
20 25 30

gca gat gcg ctg acg gag cat att tct cca gcg tat gcg cat tta att 144  
Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile  
35 40 45

gca caa gcg cag ggc gcg gac gcg cag gcg ctg aaa cgt cag gtg tgc 192  
Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys  
50 55 60

ttt gcg cca cag gag cgt gtg gtg cat gct tgc gag tgt gcc gac cca	240
Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro	
65 70 75 80	
ttg ggt gag gac cgg tac tgc gtg aca ccc ttt ttg gtg cat cag tat	288
Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr	
85 90 95	
gcg aat cgt gtg ttg atg ttg gca aca gga cgt tgc ttt tca cac tgt	336
Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys	
100 105 110	
cgc tat tgt ttt cgc cgc ggt ttc atc gcc caa cgt gca ggg tgg atc	384
Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile	
115 120 125	
ccc aac gaa gag cgc gag aag att att acg tat ctt cgt gct acc cct	432
Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro	
130 135 140	
tcg gtg aag gaa atc ctg gtt tca ggt ggt gat cca ctc act ggt tct	480
Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser	
145 150 155 160	
ttt gca cag gtc aca tcg ctt ttc cgc gca ctg cgc agt gta gcg ccg	528
Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro	
165 170 175	
gat ttg att att cgt ctg tgc act cgc gca gtc acc ttt gct ccg cag	576
Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln	
180 185 190	
gcc ttt act ccc gag ctg att gcg ttt ctg cag gag atg aag ccg gtg	624
Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val	
195 200 205	
tgg ata att ccg cat att aat cac ccg gca gag ctc ggt tct acg cag	672
Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln	
210 215 220	
cgc gcg gtg ctc gag gcc tgc gta ggc gca ggc ctc cct gtg caa tcg	720
Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser	
225 230 235 240	
cag tcg gta ctg ttg cgc ggg gtg aac gat tcg gta gag acg ctg tgc	768
Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys	
245 250 255	
aca ctg ttt cac gcg ctc act tgt ctg ggg gtt aag ccg ggg tat cta	816
Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu	
260 265 270	
ttt cag ttg gat ttg gcg cct gga act ggg gat ttt cgt gtg cca ctt	864
Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu	
275 280 285	
tct gac acg cta gct ctg tgg cgc aca ttg aag gag cgc ctc tca ggg	912
Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly	
290 295 300	
ttg tcg ctt ccc acg ctt gcg gtg gac ttg cca ggg ggt gga gga aag	960
Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Gly Lys	
305 310 315 320	

ttt ccg ctt gtg gca ttg gcc ttg cag caa gat gtc acg tgg cat cag	1008
Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln	
325 330 335	

gaa cgc gag gcg ttc tcc gca cgc ggc atc gat ggc gcg tgg tac acg	1056
Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr	
340 345 350	

tac ccg ttc	1065
Tyr Pro Phe	
355	

<210> 16  
 <211> 355  
 <212> PRT  
 <213> Treponema pallidum

<400> 16	
Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala	
1 5 10 15	
Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala	
20 25 30	
Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile	
35 40 45	
Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys	
50 55 60	
Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro	
65 70 75 80	
Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr	
85 90 95	
Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys	
100 105 110	
Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile	
115 120 125	
Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro	
130 135 140	
Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser	
145 150 155 160	
Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro	
165 170 175	
Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln	
180 185 190	
Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val	
195 200 205	
Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln	
210 215 220	
Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser	
225 230 235 240	



Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys  
                             245                            250                            255  
 Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu  
                             260                            265                            270  
 Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu  
                             275                            280                            285  
 Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly  
                             290                            295                            300  
 Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Gly Lys  
 305                            310                            315                            320  
 Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln  
                             325                            330                            335  
 Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr  
                             340                            345                            350  
 Tyr Pro Phe  
                             355

<210> 17  
 <211> 6  
 <212> PRT  
 <213> Clostridium subterminale

<400> 17  
 Lys Asp Val Ser Asp Ala  
   1                            5

<210> 18  
 <211> 17  
 <212> DNA  
 <213> Clostridium subterminale

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> n is inosine

<220>  
 <221> modified\_base  
 <222> (12)  
 <223> n is inosine

<400> 18  
 aargaygtnw sngaygc

17

<210> 19  
 <211> 6  
 <212> PRT  
 <213> Clostridium subterminale

<400> 19  
 Gln Ser His Asp Lys Val  
   1                            5

<210> 20  
 <211> 20  
 <212> DNA  
 <213> Clostridium subterminale

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> n is inosine

<220>  
 <221> modified\_base  
 <222> (15)  
 <223> n is inosine

<400> 20  
 atnacytttrt crtgnswytg

20

<210> 21  
 <211> 48  
 <212> PRT  
 <213> Clostridium subterminale

<400> 21  
 Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys Val Ile Leu Arg Asn  
 1 5 10 15

Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro Ile Asn Tyr Thr Pro  
 20 25 30

Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys Lys Val His Lys Val  
 35 40 45

<210> 22  
 <211> 15  
 <212> PRT  
 <213> Clostridium subterminale

<400> 22  
 Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln  
 1 5 10 15

<210> 23  
 <211> 16  
 <212> PRT  
 <213> Clostridium subterminale

<400> 23  
 Met Ile Asn Arg Arg Tyr Glu Leu Phe Lys Asp Val Ser Asp Ala Asp  
 1 5 10 15

<210> 24  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 24  
atcctaacga tcctaattgat cc 22

<210> 25  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 25  
tggatgggta aagtgaagtg 19

<210> 26  
<211> 500  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Probe

<400> 26  
atcctaacga tcctaattgat ccagtaagaa aacaagctat tccaacagca ttagagctta 60  
acaaagctgc tgcagatctt gaagacccat tacatgaaga tacagattca ccagtacctg 120  
gattaactca cagatatcca gatagagtat tattattaat aactgatatg tgctcaatgt 180  
actgcagaca ctgtacaaga agaagatttg caggacaaag cgatgactct atgccaatgg 240  
aaagaataga taaagctata gattatatca gaaatactcc tcaagttaga gacgtattat 300  
tatcaggtgg agacgctctt ttagtatctg atgaaacatt agaatacatc atagctaaat 360  
taagagaaat accacacggt gaaatagtaa gaatagggtc aagaactcca gttgttcttc 420  
cacaaagaat aactccagaa cttgtaaata tgcttaaaaa atatcatcca gtatgggttaa 480  
acactcactt taaccatcca 500

<210> 27  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 27  
tacacatatg ataaatagaa gatatg 26

<210> 28  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 28  
tagactcgag ttattcttga acgtgtctc 29

<210> 29  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 29  
tacagaattc atgataaata gaagatatg 29

<210> 30  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 30  
tagaaagctt ttattcttga acgtgtctc 29

<210> 31  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 31  
tataggatcc gaccgtataa ttcacgcat tacacc 36

<210> 32  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 32  
tagagaattc gattcagtca ggcgtcccat tatc 34